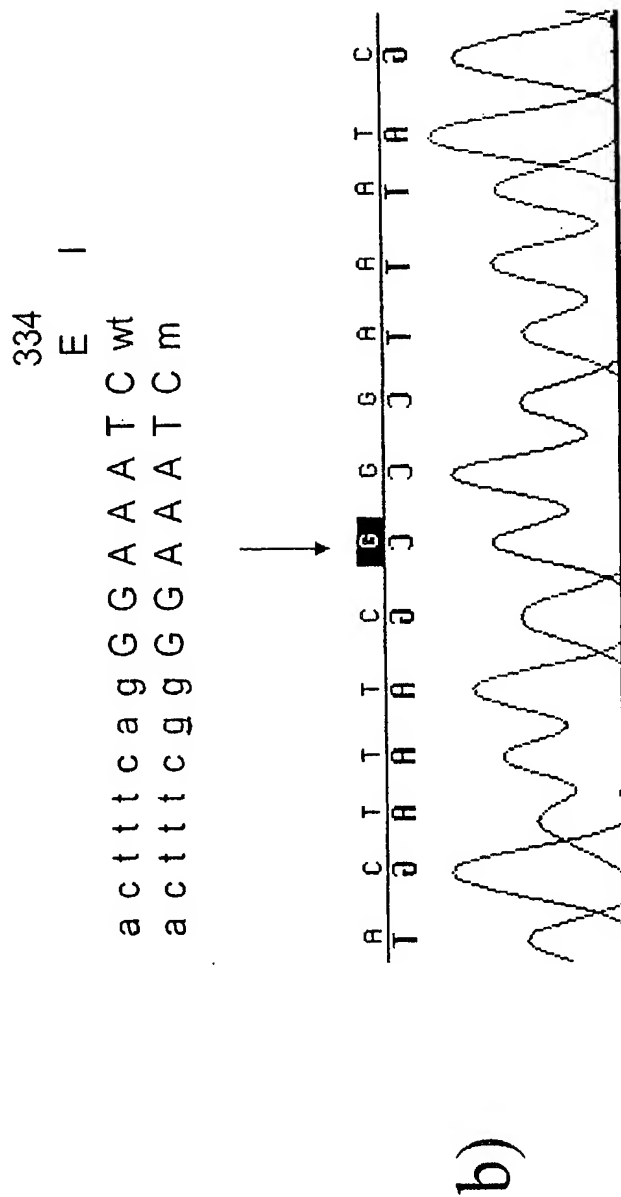
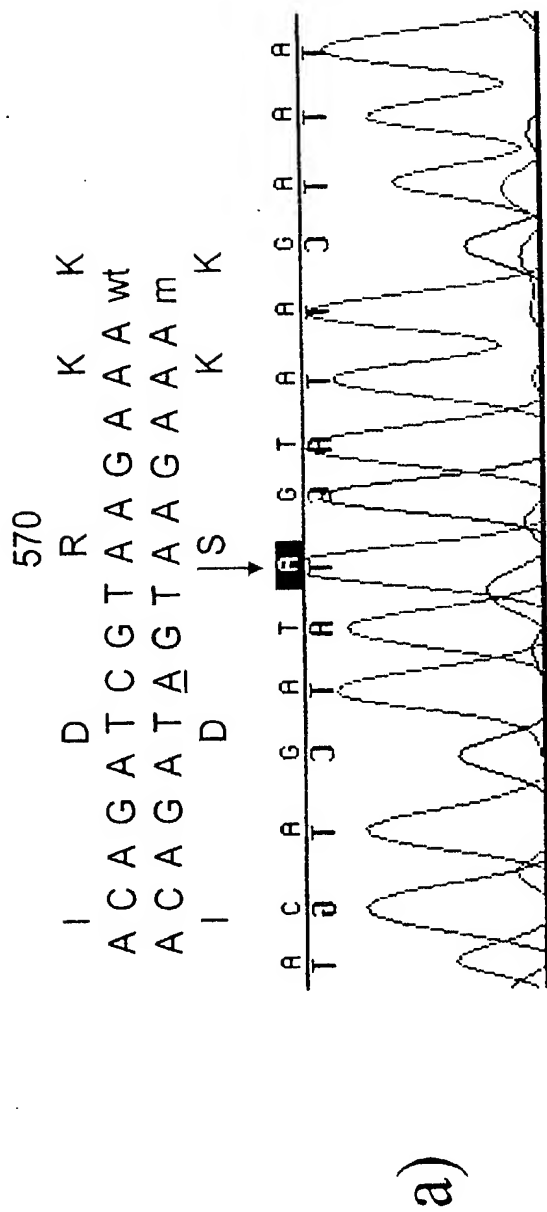
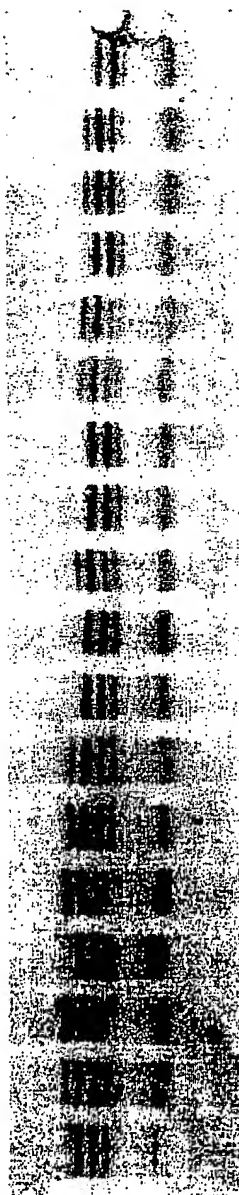
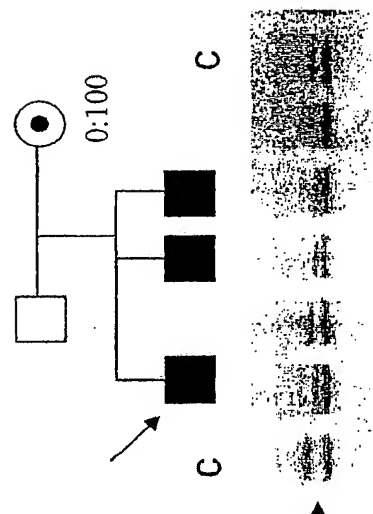


Fig. 1

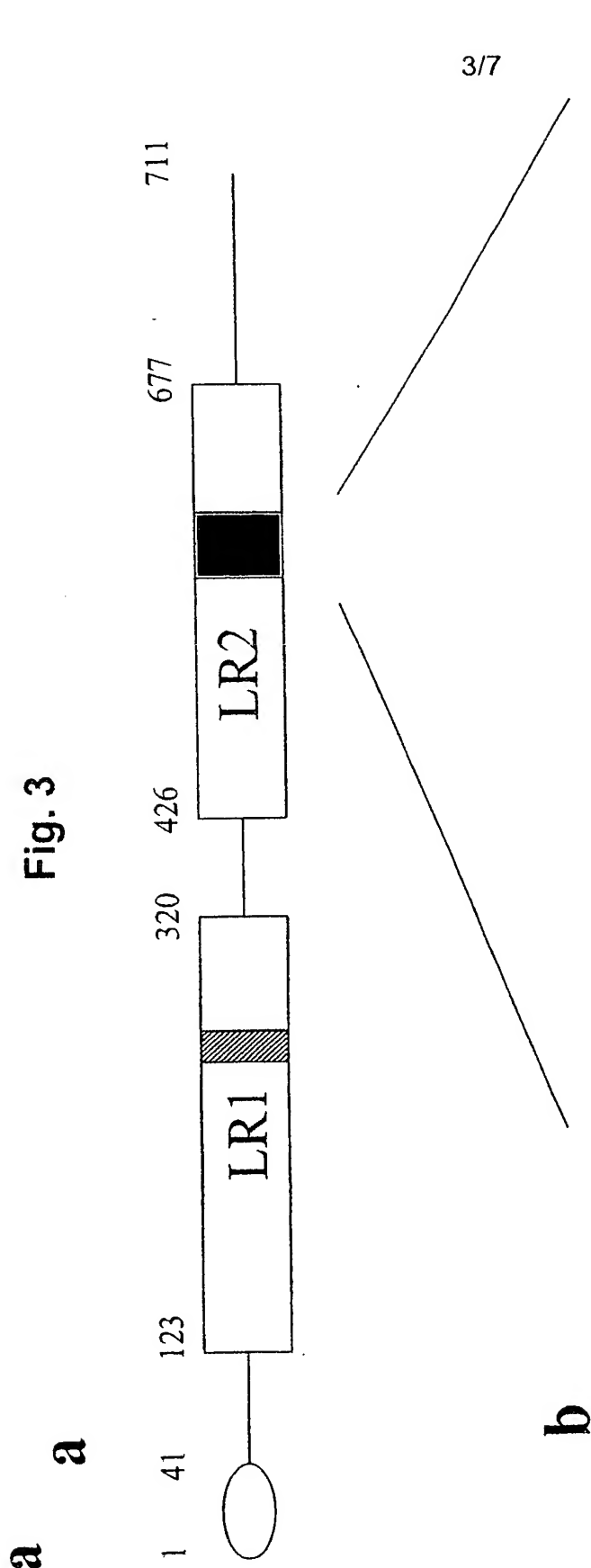




9



**BEST AVAILABLE COPY**



*FAC4* normal 546 NGQRWFCTGDIGEFHPDGC LQIIDRKK 572

*FAC4* mutant 546 NGQRWFCTGDIGEFHPDGC LQIID **S**KK 572

FACS consensus 1 DG - - **W**LH**T**GDIGXWXPXGXLKIID**R**KK 25

4/7

a) cryptic site  
actgtctccattcctttcagattattgaatatatttggtttaactttcagG Ex 11

c p  
- 318  
- 290

Fig. 4

b)

normal	Ex 10	Ex 11
--------	-------	-------

A V P E I M

mutant	Ex 10	att att gaa tat ttt gtt taa ctt tca g	Ex 11
--------	-------	---------------------------------------	-------

A V P I I E Y F V X

c)

5/7

a)

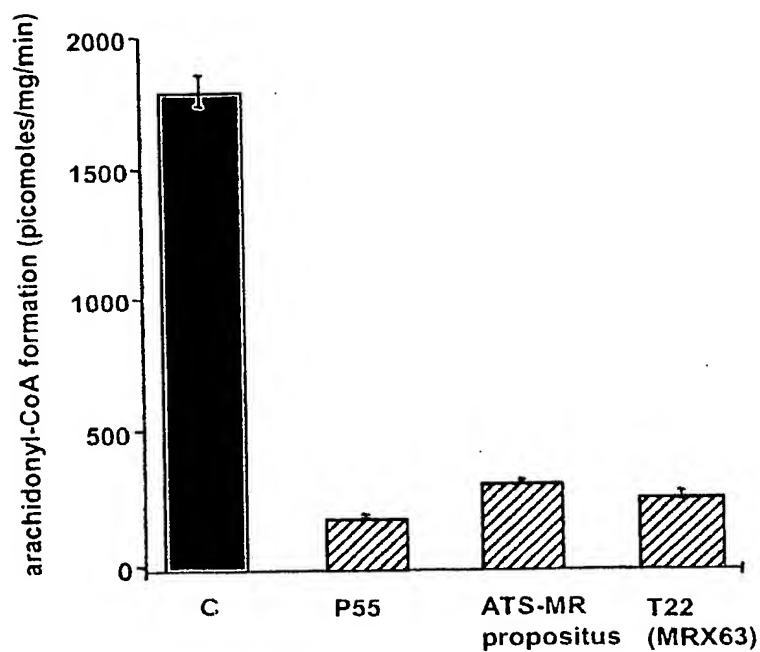
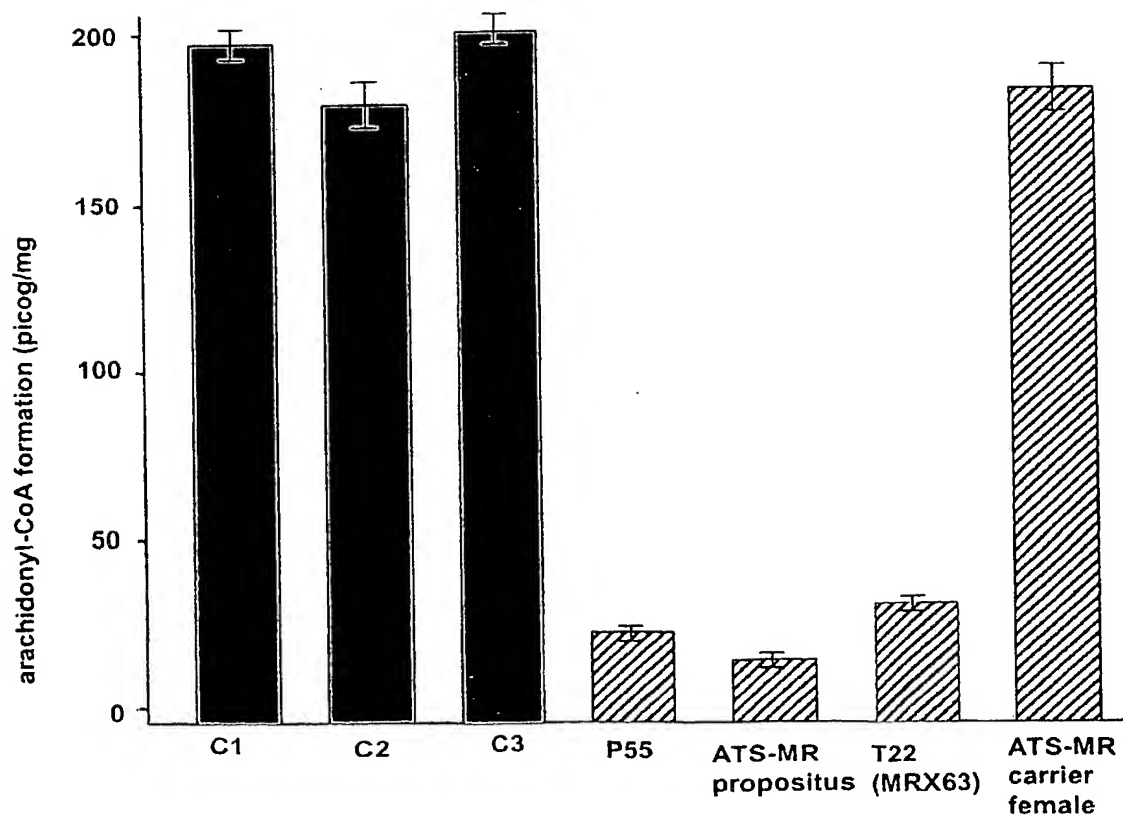


Fig. 5

b)



6/7

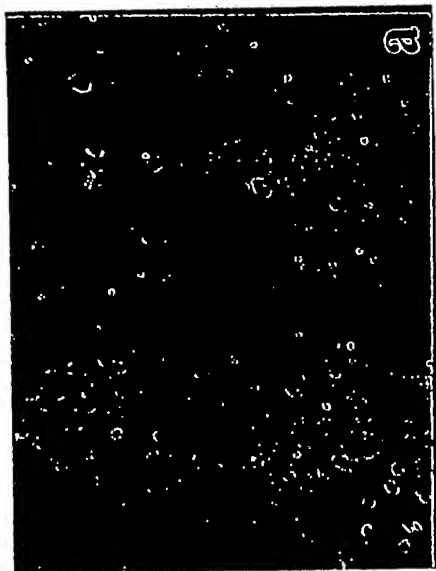
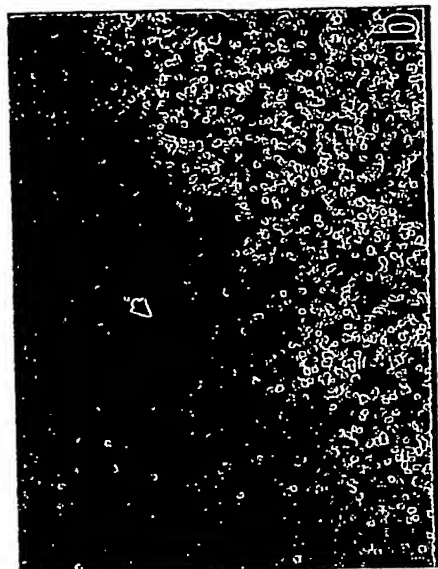


Fig. 6

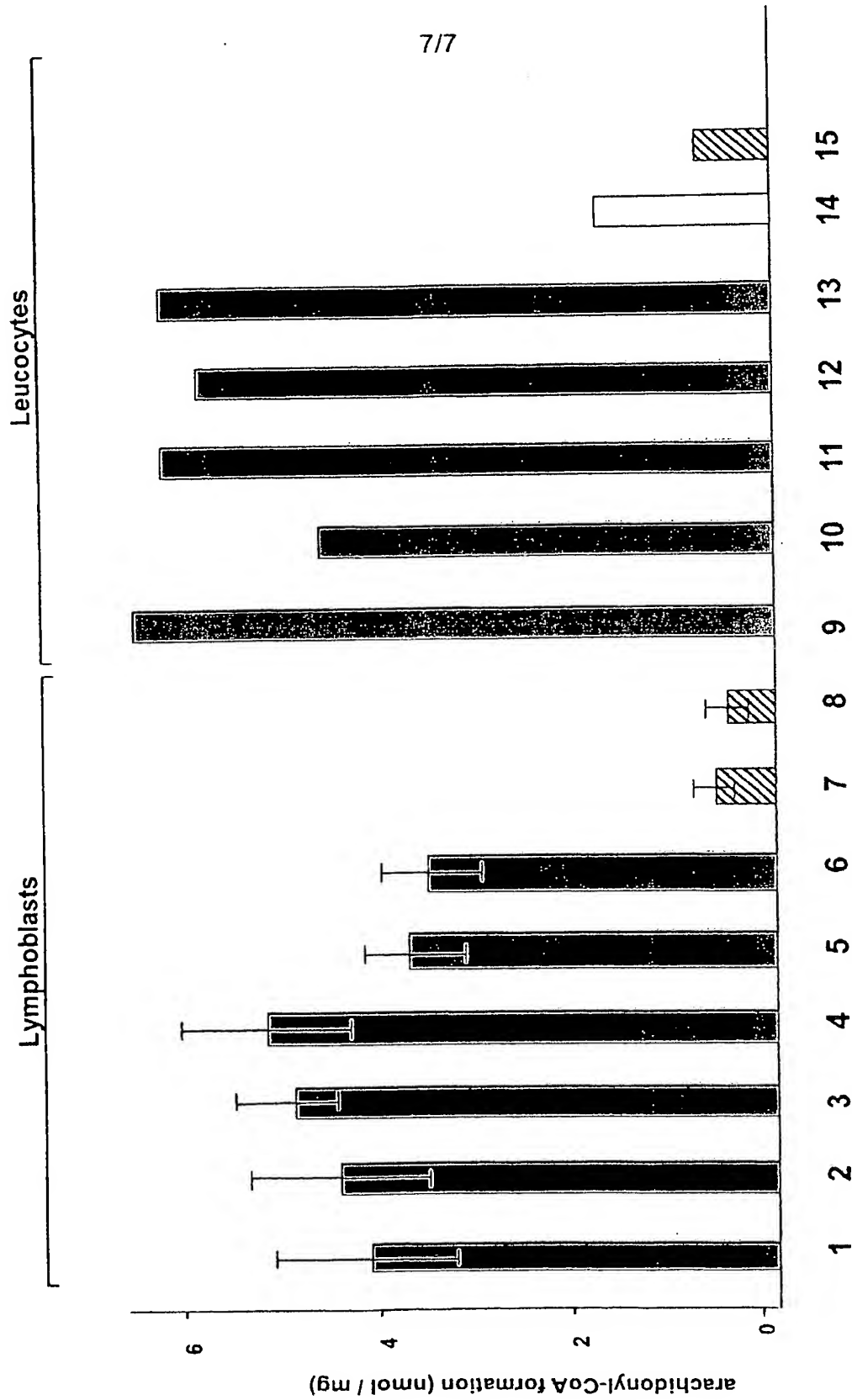


Fig. 7